

**CRF Errors Corrected by the STIC Systems Branch**

Serial Number: 09/844,861A **ENTERED**

CRF Processing Date: 11/2/2002  
 Edited by: \_\_\_\_\_  
 Verified by: [Signature] (STIC staff)

**RECEIVED**

NOV 12 2002

TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

## RAW SEQUENCE LISTING

DATE: 11/07/2002

PATENT APPLICATION: US/09/844,861A

TIME: 20:57:29

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11072002\I844861A.raw

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3 <110> APPLICANT: Padigaru, Muralidhara
4     Mishra, Vishnu
5     Spytek, Kimberly
6     Burgess, Catherine
7     Lepley, Denise
8     Grosse, William
9     Szekeres, Edward
10    Alsobrook, John
11    Gangolli, Esha
12    Casman, Stacie
13    MacDougall, John
14    Smithson, Glennnda
16 <120> TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
18 <130> FILE REFERENCE: 15966-789 US
20 <140> CURRENT APPLICATION NUMBER: 09/844,861A
21 <141> CURRENT FILING DATE: 2001-04-27
23 <150> PRIOR APPLICATION NUMBER: 60/199,947
24 <151> PRIOR FILING DATE: 2000-04-27
26 <150> PRIOR APPLICATION NUMBER: 60/199,960
27 <151> PRIOR FILING DATE: 2000-04-27
29 <150> PRIOR APPLICATION NUMBER: 60/225,226
30 <151> PRIOR FILING DATE: 2000-08-14
32 <150> PRIOR APPLICATION NUMBER: 60/256,399
33 <151> PRIOR FILING DATE: 2000-12-18
35 <150> PRIOR APPLICATION NUMBER: 60/256,524
36 <151> PRIOR FILING DATE: 2000-12-18
38 <150> PRIOR APPLICATION NUMBER: 60/258,159
39 <151> PRIOR FILING DATE: 2000-12-22
41 <150> PRIOR APPLICATION NUMBER: 60/258,511
42 <151> PRIOR FILING DATE: 2000-12-28
44 <150> PRIOR APPLICATION NUMBER: 60/258,828
45 <151> PRIOR FILING DATE: 2000-12-28
47 <150> PRIOR APPLICATION NUMBER: 60/259,659
48 <151> PRIOR FILING DATE: 2001-01-04
50 <150> PRIOR APPLICATION NUMBER: 60/275,604
51 <151> PRIOR FILING DATE: 2001-03-13
53 <160> NUMBER OF SEQ ID NOS: 113
55 <170> SOFTWARE: PatentIn Ver. 2.1
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58 <211> LENGTH: 1016
59 <212> TYPE: DNA
60 <213> ORGANISM: Homo sapiens
62 <400> SEQUENCE: 1

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65 agcccttcta gggaaacatca ttatcctggt tgtgatacag actgaacaga gcctccacca 180
66 acccatgttt tacttcctag ccatgttggc cggcactgat ctgggcttgt ctacagcaac 240
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70 caacaaggta atagccattc tgggcatagt catcattgtc aggactttgg tatttgtgac 480
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73 attgattgcc ttctcagtgg gatacattga catttctgtg attggatttt cctatgtcca 660
74 gatcctccga gctgtcttcc atctcccagc ctgggatgcc cggcttaagg cactcagcac 720
75 atgtggctct cacgtctgtg ttatgttggc tttctacctg ccagccctct tttccttcat 780
76 gacacaccgc tttggccaca acatccctca ttacatccac attcttctgg ccaatctgta 840
77 tgtggttttt cccctgctc ttaactctgt tatctatggg gtcaaaacaa aacagatacg 900
78 agagcaggta cttaggatac tcaaccctaa aagcttttgg cattttgacc ccaagaggat 960
79 cttccacaac aattcagttg acaaattgaga tcataacaaa ataaacactg gaaaca 1016

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83 &lt;211&gt; LENGTH: 327

84 &lt;212&gt; TYPE: PRT

85 &lt;213&gt; ORGANISM: Homo sapiens

87 &lt;400&gt; SEQUENCE: 2

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91 Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
92           20           25           30
94 Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Ile Leu
95           35           40           45
97 Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
98   50           55           60
100 Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
101  65           70           75           80
103 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
104           85           90           95
106 Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
107           100          105          110
109 Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
110          115          120          125
112 Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
113          130          135          140
115 Ile Leu Gly Ile Val Ile Val Arg Thr Leu Val Phe Val Thr Pro
116 145          150          155          160
118 Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
119          165          170          175
121 Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
122          180          185          190
124 Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
125          195          200          205
127 Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val

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128      210      215      220
130 Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
131 225      230      235      240
133 Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
134      245      250      255
136 Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
137      260      265      270
139 Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
140      275      280      285
142 Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
143      290      295      300
145 Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
146 305      310      315      320
148 His Asn Asn Ser Val Asp Lys
149      325
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153 <211> LENGTH: 1121
154 <212> TYPE: DNA
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 3
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159 tgtcagccat catgtctggg gacaacagct ccagcctgac cccaggattc tttatcttga 120
160 atggcgttcc tgggctggaa gccacacaca tctggatctc cctgccattc tgctttatgt 180
161 acatcattgc tgtcgtgggg aactgtgggc tcatctgcct catcagccat gaggaggccc 240
162 tgcaccggcc catgtactac ttctggccc tgctctcctt cactgatgtc acctgttgca 300
163 ccaccatggt acctaatatg ctgtgcatat tctggttcaa cctcaaggag attgacttta 360
164 acgcctgcct ggcccagatg ttttttgtcc atatgctgac agggatggag tctgggggtgc 420
165 tcatgctcat ggccctggac cgctatgtgg ccatctgcta ccccttacgc tatgccacca 480
166 tccttaccaa ccctgtcatc gccaaggctg gtcttgccac cttcttgagg aatgtgatgc 540
167 tcatcatccc attcactctc ctcaccaagc gcctgcccta ttgccggggg aacttcatcc 600
168 cccacaccta ctgtgaccat atgtctgtgg ccaaggatc ctgtggcaat ttcaagggtca 660
169 atgtatttta tggctgatg gttgctctcc tgattggtgt gtttgatata tgctgtatct 720
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171 acaaagcctt cagcaccctg acatctcaca tgtgttccat tgtgatcacc tatgttgctg 840
172 cttttttcac ttttttcaact catcgttttg taggacacaa tatcccaaac cacatacaca 900
173 tcatcgtagc caacctttat ctgctactgc ctctaccat gaacccaatt gtttatggag 960
174 tcaagaccaa gcagattcag gaagggtgaa ttaaatTTTT acttgaggac aagggttagtt 1020
175 ttacctatga caaatgaaac atagaataga catattgttt caggtggtga gaaaataatg 1080
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180 <211> LENGTH: 336
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 4
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188 Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu Asn
189      20      25      30
191 Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro Phe

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192          35          40          45
194 Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile Cys
195          50          55          60
197 Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe Leu
198 65          70          75          80
200 Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val Pro
201          85          90          95
203 Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe Asn
204          100          105          110
206 Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met Glu
207          115          120          125
209 Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile Cys
210          130          135          140
212 Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala Lys
213 145          150          155          160
215 Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro Phe
216          165          170          175
218 Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile Pro
219          180          185          190
221 His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly Asn
222          195          200          205
224 Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile Gly
225          210          215          220
227 Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu Gln
228 225          230          235          240
230 Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe Ser
231          245          250          255
233 Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala Ala
234          260          265          270
236 Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro Asn
237          275          280          285
239 His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro Thr
240          290          295          300
242 Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu Gly
243 305          310          315          320
245 Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp Lys
246          325          330          335

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253 &lt;211&gt; LENGTH: 1050

254 &lt;212&gt; TYPE: DNA

255 &lt;213&gt; ORGANISM: Homo sapiens

257 &lt;400&gt; SEQUENCE: 5

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259 tcattttctaa atggcaccag cctaactcca gcttcattca tcctaaatgg catccctggg 120
260 ttggaagatg tgcatttgtg gatctccttc ccactgtgta ccatgtacag cattgctatt 180
261 acaggggaact tcggccttat gtacctcatc tactgtgatg aggccttaca cagacctatg 240
262 tatgtcttcc ttgcccttct ttccctcaca gatgtgctca tgtgcaccag cacccttccc 300
263 aacactctct tcatattgtg gtttaatctc aaggagattg attttaaagc ctgcctcgcc 360
264 cagatgttct ttgtgcacac cttcacaggg atggagtctg ggggtgctcat gctcatggcc 420

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265 ctggaccact gtgtggccat ctgcttccct ctgcgttatg ccaccatcct cactaattca 480
266 gtcattgcta aagctgggtt cctcactttt cttaggggtg tgatgcttgt tatcccttcc 540
267 actttcctca ccaagcgctt tccatactgc aagggcaacg tcatacccca cacctactgt 600
268 gaccacatgt ctgtggccaa gatattctgt ggtaatgtca gggttaacgc catctatggt 660
269 ttgatagttg ccctgctgat tgggggcttt gatatcctgt gcattacaat ctctacact 720
270 atgattcttc aagcagttgt gagtctatca tcagcagatg ctgcacagaa ggccttcagc 780
271 acctgcactg cccacttctg tgccatagtc ctcacctatg ttccagcctt ctttaccttc 840
272 tttacacacc attttggggg acacaccatt cctctacaca tacatattat tatggctaata 900
273 ctctacctac taatgcctcc cacaatgaac cctattgtgt atggggtgaa aaccaggcag 960
274 gtacgagaaa gtgtcattag gttctttctt aagggaagg acaattctca taacttttaa 1020
275 agtcttctga gatgtagaa ttttcttagc 1050
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279 <211> LENGTH: 320
280 <212> TYPE: PRT
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 6
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287 Asn Gly Ile Pro Gly Leu Glu Asp Val His Leu Trp Ile Ser Phe Pro
288 20 25 30
290 Leu Cys Thr Met Tyr Ser Ile Ala Ile Thr Gly Asn Phe Gly Leu Met
291 35 40 45
293 Tyr Leu Ile Tyr Cys Asp Glu Ala Leu His Arg Pro Met Tyr Val Phe
294 50 55 60
296 Leu Ala Leu Leu Ser Phe Thr Asp Val Leu Met Cys Thr Ser Thr Leu
297 65 70 75 80
299 Pro Asn Thr Leu Phe Ile Leu Trp Phe Asn Leu Lys Glu Ile Asp Phe
300 85 90 95
302 Lys Ala Cys Leu Ala Gln Met Phe Phe Val His Thr Phe Thr Gly Met
303 100 105 110
305 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp His Cys Val Ala Ile
306 115 120 125
308 Cys Phe Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Ser Val Ile Ala
309 130 135 140
311 Lys Ala Gly Phe Leu Thr Phe Leu Arg Gly Val Met Leu Val Ile Pro
312 145 150 155 160
314 Ser Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Lys Gly Asn Val Ile
315 165 170 175
317 Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly
318 180 185 190
320 Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile
321 195 200 205
323 Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
324 210 215 220
326 Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
327 225 230 235 240
329 Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro
330 245 250 255
332 Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro

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VERIFICATION SUMMARY

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